

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2003, 15:40:19 ; Search time 21 Seconds
(without alignments)
566.160 Million cell updates/sec

Title: US-09-991-209-2
Perfect score: 1492
Sequence: 1 MKQFSKXHLVAVVTAGHAL.....QGVNNAHTTYGMTSGACTW 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pdp:*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pdp:*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pdp:*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pdp:*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pdp:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pdp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1492	100.0	281	4	US-08-952-445-28 Sequence 28, Appl
2	1026	68.8	197	4	US-08-952-445-26 Sequence 26, Appl
3	403	27.0	77	3	US-08-975-600-7 Sequence 7, Appl
4	362	24.3	289	4	US-09-007-288E-145 Sequence 145, Appl
5	353.5	23.7	291	1	US-08-434-255-13 Sequence 13, Appl
6	353.5	23.7	291	1	US-08-459-967-13 Sequence 13, Appl
7	353.5	23.7	291	1	US-08-460-327-13 Sequence 13, Appl
8	353.5	23.7	291	1	US-08-459-871-13 Sequence 13, Appl
9	353.5	23.7	291	1	US-08-244-686-4 Sequence 4, Appl
10	353.5	23.7	291	2	US-08-784-651-16 Sequence 16, Appl
11	353.5	23.7	291	2	US-08-921-426-10 Sequence 10, Appl
12	353.5	23.7	291	2	US-08-479-275D-2 Sequence 2, Appl
13	353.5	23.7	291	2	US-08-488-271B-2 Sequence 2, Appl
14	353.5	23.7	291	2	US-08-140-008A-2 Sequence 2, Appl
15	353.5	23.7	291	2	US-08-701-339-2 Sequence 2, Appl
16	353.5	23.7	291	3	US-08-816-915-10 Sequence 10, Appl
17	353.5	23.7	291	3	US-09-024-532-6 Sequence 6, Appl
18	353.5	23.7	291	4	US-09-007-288E-16 Sequence 16, Appl
19	353.5	23.7	291	5	PCT-US95-07743-10 Sequence 10, Appl
20	353.5	23.7	384	4	US-09-295-744A-14 Sequence 14, Appl
21	351.5	23.6	294	4	US-09-007-288E-142 Sequence 142, Appl
22	351.5	23.6	294	4	US-09-007-288E-143 Sequence 143, Appl
23	349	23.4	270	3	US-08-362-525-8 Sequence 8, Appl
24	334	22.4	363	2	US-08-784-651-15 Sequence 15, Appl
25	334	22.4	363	4	US-09-402-664A-11 Sequence 11, Appl
26	328	22.0	269	3	US-09-111-556A-4 Sequence 4, Appl
27	328	22.0	269	3	US-08-360-758-4 Sequence 4, Appl

28	323.5	21.7	297	2	US-08-859-106A-2	Sequence 2, Appl
29	323.5	21.7	297	4	US-09-402-664A-9	Sequence 9, Appl
30	317.5	21.3	297	3	US-09-142-469-2	Sequence 2, Appl
31	307.5	20.6	329	4	US-09-892-074-2	Sequence 2, Appl
32	305	20.4	305	4	US-09-402-664A-12	Sequence 12, Appl
33	305	20.4	349	4	US-09-703-416-2	Sequence 2, Appl
34	305	20.4	349	4	US-09-703-414-2	Sequence 2, Appl
35	301	20.2	350	4	US-09-892-188B-2	Sequence 2, Appl
36	297	19.9	337	2	US-08-784-651-8	Sequence 8, Appl
37	297	19.9	338	2	US-08-784-651-10	Sequence 10, Appl
38	292	19.6	338	2	US-08-784-651-6	Sequence 6, Appl
39	290	19.4	297	3	US-09-111-556A-5	Sequence 5, Appl
40	290	19.4	297	3	US-08-360-758-5	Sequence 5, Appl
41	290	19.4	333	3	US-08-988-111-3	Sequence 3, Appl
42	290	19.4	333	3	US-09-387-922-3	Sequence 3, Appl
43	290	19.4	392	4	US-09-402-664A-10	Sequence 10, Appl
44	290	19.4	392	6	5219753-2	Patent No. 5219753
45	289.5	19.4	336	2	US-08-784-651-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-952-445-28
; Sequence 28, Application US/08952445
; Patent No. 6368833
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: ESTERASE ENZYMES, DNA ENCODING
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International, Inc.
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/952,445
; FILING DATE: 18-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/722,713
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Stone, Christopher L.
; REGISTRATION NUMBER: 35,696
; REFERENCE/DOCKET NUMBER: GCJ62-2-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-846-7555
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-952-445-28

Query Match 100.0%; Score 1492; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 4.6e-147; Indels 0; Gaps 0;
Matches 281; Conservative 0; Mismatches 0;
Oy 1 MKQFSKXHLVAVVTAGHALAASTGISEDYSLRVEMATISQAAVADLCNIPSTIKGE 60
Db 1 MKQFSKXHLVAVVTAGHALAASTGISEDYSLRVEMATISQAAVADLCNIPSTIKGE 60

RESULT 3

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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Query Match	27.0%	Score 403;	DB 3;	Length 77;
Best Local Similarity	94.8%;	Pred. No. 1.4e-34;		
Matches 73; Conservative	2;	Mismatches 2;	Indels 0;	Gaps 0
Qy 69	INGWILRDDSSKIIIVFRGTGSDTNLQLDNTYLTLPFDTLPCQCNCVHGYYIGWVSV	128		

Query Match	27.0%;	Score 403;	
Best Local Similarity	94.8%;	Pred. No. 1.1.	
Matches 73; Conservative	2;	Mismatch	
Qy	69	INGMILRRDSSKEIITVPRGTGSDTNLQDNTN	
Db	1	INGMILRRDTSKEIITVPRGTGSDTNLQDNTN	
Qy	129	QDQVESLVKQVQSQYPD 145	
Db	61	QDQVESLVKQASQYPD 77	
RESULT 4			
US-09-007-288E-145			
; Sequence 145, Application US/09007288E			
; Patent No. 6495357			
; GENERAL INFORMATION:			
; APPLICANT: Fugisang, Claus			
; APPLICANT: Okkels, Jens			
; APPLICANT: Petersen, Dorte			

APPLICANT: Patkar, Shankar
APPLICANT: Thellersen, Marianne
APPLICANT: Svenden, Allan
APPLICANT: Borch, Kim
APPLICANT: Royer, John
APPLICANT: Kretschmar, Titus
APPLICANT: Halkier, Torben
APPLICANT: Vind, Jesper
APPLICANT: Jorgensen, Steen
TITLE OF INVENTION: No. 6495357el Lipolytic Enzymes
FILE REFERENCE: 4455-404-US
CURRENT APPLICATION NUMBER: US/09/007,288E
CURRENT FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PatentIn version 3.1
SEQ ID NO 145
LENGTH: 289
TYPE: PRT
ORGANISM: Humicola lanuginosa lipase
US-09-007-288E-145

Query Match 24.3%; Score 362; DB 4; Length 289;
Best Local Similarity 30.2%; Pred. No. 2e-29;
Matches 92; Conservative 58; Mismatches 105; Indels 50; Gaps 11;
QY 7 KHLVAVVVTAGHALAASQTGISEDLYSRLVEMATISOAAAYADL-----CNIPST----- 55
DB 2 KRCCGSLLLGLSISALAEVSQLFNQNLFAQYSAAYCGKNDAPAGTNICTGNAC 61
QY 56 --TIKGEKYY-----NSQTDINGWILRDDSSKEIITVFRGTGSDTNQLDNTNYTLTPFD 107
DB 62 PEVEKADATFLYSPEDSGVGVDTGFLADNTNKLIVLSFRGSRSIENWGNLNPDLKEIN 121
QY 108 TLPQCNCCEVHGYYIGWVSQDOVESLVKQVQYDPDYALTVTGHSIGASLAALTAQOL 167
DB 122 DI--CSCRGHDGFTSWRSVADTLROKVEDAVREHPDYRVVFTGHSIGGALATVAGADL 179
QY 168 SATVDNRLRTFTGPRSGNOAFASYMNDAFQASSPDITQ-----YFRVTHANDGIPNLPVPV 223
DB 180 RGNGYDIDVSYGAPRVGNRAFAEFL-----TVQTGGLYRIIHTNDIVRPLPPR 229
QY 224 EQGYAHGVEYV-----SVDPYSAQNTFVCTGDEVCCEAQQGQGVNN-----AHTTYFGM 274
DB 230 EFGVSHSSPEWIKSGTLVPVT-RNDIV-----KIEGIDATGNNQNPIDIPAHLWYFGL 284
QY 275 TSGAC 279
DB 285 I-GTC 288

RESULT 5
US-08-434-255-13
Sequence 13, Application US/08434255
Patent No. 5621089
GENERAL INFORMATION:
APPLICANT: Sloma, Alan P.
APPLICANT: Outtrup, Helle
APPLICANT: Dambmann, Claus
APPLICANT: Aaslyng, Dorrit
TITLE OF INVENTION: ALKALINE PROTEASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5621089o No. 5621089disk of No. 5621089th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,255
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Agria Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3764.400-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-434-255-13
Query Match 23.7%; Score 353.5; DB 1; Length 291;
Best Local Similarity 31.4%; Pred. No. 1.6e-28;
Matches 94; Conservative 54; Mismatches 100; Indels 51; Gaps 12;
QY 14 VTAGHALAAS-TQGISDLYSRLVEMATISOAAAYADL-----CNIPST-----IIKG 59
DB 10 VSAWTALASPIRREVSQLFNQNLFAQYSAAYCGKNDAPAGTNICTGNACPEVEKA 69
QY 60 EKIY-----NSQTDINGWILRDDSSKEIITVFRGTGSDTNQLDNTNYTLTPFDLPOCN 113
DB 70 DATFLYSPEDSGVGVDTGFLADNTNKLIVLSFRGSRSIENWGNLNPDLKEINDI--CS 127
QY 114 GCEVHGYYIGWVSQDOVESLVKQVQYDPDYALTVTGHSIGASLAALTAQOLSATYDN 173
DB 128 GCRGHDGFTSWRSVADTLROKVEDAVREHPDYRVVFTGHSIGGALATVAGADLRNGYD 187
QY 174 IRLTYFGPRSGNOAFASYMNDAFQASSPDITQ-----YFRVTHANDGIPNLPPEQGYAH 229
DB 188 IDVSYGAPRVGNRAFAEFL-----TVQTGGLYRIIHTNDIVRPLPPREFGYSH 237
QY 230 GGYEYV-----SVDPYSAQNTFVCTGDEVCCEAQQGQGVNN-----AHTTYFGMTSGAC 279
DB 238 SSPEYWKSGTLVPVT-RNDIV-----KIEGIDATGNNQNPIDIPAHLWYFGLI-GTC 290

RESULT 6
US-08-459-967-13
Sequence 13, Application US/08459967
Patent No. 5622841
GENERAL INFORMATION:
APPLICANT: Sloma, Alan P.
APPLICANT: Outtrup, Helle
APPLICANT: Dambmann, Claus
APPLICANT: Aaslyng, Dorrit
TITLE OF INVENTION: ALKALINE PROTEASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5622841o No. 5622841disk of No. 5622841th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,967
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/434,255

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; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Agris Dr., Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 3764.400-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-967-13

Query Match      23.7%; Score 353.5; DB 1; Length 291;
Best Local Similarity 31.4%; Pred. No. 1.6e-28;
Matches 94; Conservative 54; Mismatches 100; Indels 51; Gaps 12;

QY 14 VTAGHALAAS-TQGISSELYSLVEMATISQAAYADL-----CNIPST-----IIKG 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 10 VSAWTAASPIRREVSQDLFNQFNLFPAQYSAAYCGKNDAPAGTNICTGNACPEVEKA 69
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 EKII-----NSQDINGHILDDSSKEIITVPRGTGSDTNLQDNTYTLTPDTPQCN 113
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 70 DATFLYSPEDSGVGTGFLADNTNKLIVLSFRGSRSIENWGNLNFDLKEINDI--CS 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 114 GCEVHGYYIGWVSQDOVESLVKQVQSYDPYALVTGHSGLASLAALTAQOLSATYDN 173
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 GCRGHDGFTSSWRSVADTLRQKVEDAVREHPDYRVVFTGHSGLGALATVAGADLRNGYD 187
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 174 IRLYTFGEPRSGNQAFASYNDAFAQSSPDTTQ-----YFRVTHANDGIPNLPPVEQGYAH 229
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 188 IDVFSYGAPRVGNRAFAEFL-----TVQTGGTLRYITHNDIVPRLPREFGYSH 237
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 230 GGVEYH-----SVDPSAQTFTVCTGDEVQCCAAQGGGVNN-----AHTTYFGMTSGAC 279
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 238 SSPEYWKSGTLVPVT-RNDIV-----KIEGIDATGNNQNPIDIPAHLYWFGLI-GTC 290

RESULT 7
US-08-460-327-13
; Sequence 13, Application US/08460327
; Patent No. 5622850
; GENERAL INFORMATION:
; APPLICANT: Sloma, Alan P.
; APPLICANT: Outtrup, Helle
; APPLICANT: Dammann, Claus
; APPLICANT: Asalyng, Dorrit
; TITLE OF INVENTION: ALKALINE PROTEASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5622850 No. 5622850disk of No. 5622850th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,327
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/434,255
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Agris Dr., Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 3764.400-US
; TELECOMMUNICATION INFORMATION:

; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Agris Dr., Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 3764.400-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-967-13

Query Match      23.7%; Score 353.5; DB 1; Length 291;
Best Local Similarity 31.4%; Pred. No. 1.6e-28;
Matches 94; Conservative 54; Mismatches 100; Indels 51; Gaps 12;

QY 14 VTAGHALAAS-TQGISSELYSLVEMATISQAAYADL-----CNIPST-----IIKG 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 10 VSAWTAASPIRREVSQDLFNQFNLFPAQYSAAYCGKNDAPAGTNICTGNACPEVEKA 69
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 EKII-----NSQDINGHILDDSSKEIITVPRGTGSDTNLQDNTYTLTPDTPQCN 113
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 70 DATFLYSPEDSGVGTGFLADNTNKLIVLSFRGSRSIENWGNLNFDLKEINDI--CS 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 114 GCEVHGYYIGWVSQDOVESLVKQVQSYDPYALVTGHSGLASLAALTAQOLSATYDN 173
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 GCRGHDGFTSSWRSVADTLRQKVEDAVREHPDYRVVFTGHSGLGALATVAGADLRNGYD 187
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 174 IRLYTFGEPRSGNQAFASYNDAFAQSSPDTTQ-----YFRVTHANDGIPNLPPVEQGYAH 229
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 188 IDVFSYGAPRVGNRAFAEFL-----TVQTGGTLRYITHNDIVPRLPREFGYSH 237
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 230 GGVEYH-----SVDPSAQTFTVCTGDEVQCCAAQGGGVNN-----AHTTYFGMTSGAC 279
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 238 SSPEYWKSGTLVPVT-RNDIV-----KIEGIDATGNNQNPIDIPAHLYWFGLI-GTC 290

RESULT 8
US-08-459-871-13
; Sequence 13, Application US/08459871
; Patent No. 5650326
; GENERAL INFORMATION:
; APPLICANT: Sloma, Alan P.
; APPLICANT: Outtrup, Helle
; APPLICANT: Dammann, Claus
; APPLICANT: Asalyng, Dorrit
; TITLE OF INVENTION: ALKALINE PROTEASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5650326 No. 5650326disk of No. 5650326th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,871
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/434,255
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Agris Dr., Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 3764.400-US
; TELECOMMUNICATION INFORMATION:
```

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/ TELEPHONE: 212-867-0123
/ TELEFAX: 212-878-9655
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 291 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-459-871-13

Query Match      23.7%; Score 353.5; DB 1; Length 291;
Best Local Similarity 31.4%; Pred. No. 1.6e-28;
Matches 94; Conservative 54; Mismatches 100; Indels 51; Gaps 12;

QY 14 VTAGHALAAS-TQGISDLYSLRLEMATISQAAYADL-----CNIPST-----IIKG 59
DB 10 VSAWTALASPIRREVSDQFNQNLFAQYSAAYCGKNNDAPAGTNICTGNACPEVEKA 69
QY 60 EKIV-----NSQTDINGWILRDDSSKEIITVFRGTGSDTNLQDNTYTLTPFDLPQCN 113
DB 70 DATFLYSFEDSGVDVTGFLALDNTKLI VLSFRGSRSIENWGNLFDLKEINDI--CS 127
QY 114 GCEVHGYYIGWVSQVQVESLVKQOVSQYDPDYALTVTGHSLSGLASLAALTAQOLSATYDN 173
DB 128 GCRGHDGFTSSWRSVADTLROKVEDAVREHPDYRVVFTGHSLSGLGALATVAGADLRNGYD 187
QY 174 IRLYTFGEPRSGNOAFASYMNDAPQASSPDITQ-----YFRVTHANDGIPNLPPEQGYAH 229
DB 188 IDVFSYGAPRVGNRAFAEFL-----TVQTGGTLRYITHNTDIVRPLPPREFGYSH 237
QY 230 GGVEYW-----SVDPSYAQNTFVCTGDEVQCEAQQGGVNN-----AHTTYFGMTSGAC 279
DB 238 SSPEYIKSGTLVPVT-RNDIV-----KIEGIDATGNNQNPIDIPAHLWTFGLI-GTC 290

RESULT 9
US-08-244-686-4
/ Sequence 4, Application US/08244686
/ Patent No. 5703358
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: Process for the production of a protein
/ TITLE OF INVENTION: using endoxylanase II (exII) expression signals
/ NUMBER OF SEQUENCES: 12
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/244,686
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 291 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-244-686-4

Query Match      23.7%; Score 353.5; DB 1; Length 291;
Best Local Similarity 31.4%; Pred. No. 1.6e-28;
Matches 94; Conservative 54; Mismatches 100; Indels 51; Gaps 12;

QY 14 VTAGHALAAS-TQGISDLYSLRLEMATISQAAYADL-----CNIPST-----IIKG 59
DB 10 VSAWTALASPIRREVSDQFNQNLFAQYSAAYCGKNNDAPAGTNICTGNACPEVEKA 69
QY 60 EKIV-----NSQTDINGWILRDDSSKEIITVFRGTGSDTNLQDNTYTLTPFDLPQCN 113
DB 70 DATFLYSFEDSGVDVTGFLALDNTKLI VLSFRGSRSIENWGNLFDLKEINDI--CS 127
QY 114 GCEVHGYYIGWVSQVQVESLVKQOVSQYDPDYALTVTGHSLSGLASLAALTAQOLSATYDN 173
DB 128 GCRGHDGFTSSWRSVADTLROKVEDAVREHPDYRVVFTGHSLSGLGALATVAGADLRNGYD 187
QY 174 IRLYTFGEPRSGNOAFASYMNDAPQASSPDITQ-----YFRVTHANDGIPNLPPEQGYAH 229
DB 188 IDVFSYGAPRVGNRAFAEFL-----TVQTGGTLRYITHNTDIVRPLPPREFGYSH 237
QY 230 GGVEYW-----SVDPSYAQNTFVCTGDEVQCEAQQGGVNN-----AHTTYFGMTSGAC 279
DB 238 SSPEYIKSGTLVPVT-RNDIV-----KIEGIDATGNNQNPIDIPAHLWTFGLI-GTC 290

RESULT 9
US-08-244-686-4
/ Sequence 4, Application US/08244686
/ Patent No. 5703358
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: Process for the production of a protein
/ TITLE OF INVENTION: using endoxylanase II (exII) expression signals
/ NUMBER OF SEQUENCES: 12
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/244,686
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 291 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-244-686-4

Query Match      23.7%; Score 353.5; DB 2; Length 291;
Best Local Similarity 31.4%; Pred. No. 1.6e-28;
Matches 94; Conservative 54; Mismatches 100; Indels 51; Gaps 12;

QY 14 VTAGHALAAS-TQGISDLYSLRLEMATISQAAYADL-----CNIPST-----IIKG 59
DB 10 VSAWTALASPIRREVSDQFNQNLFAQYSAAYCGKNNDAPAGTNICTGNACPEVEKA 69
QY 60 EKIV-----NSQTDINGWILRDDSSKEIITVFRGTGSDTNLQDNTYTLTPFDLPQCN 113
DB 70 DATFLYSFEDSGVDVTGFLALDNTKLI VLSFRGSRSIENWGNLFDLKEINDI--CS 127
QY 114 GCEVHGYYIGWVSQVQVESLVKQOVSQYDPDYALTVTGHSLSGLASLAALTAQOLSATYDN 173
DB 128 GCRGHDGFTSSWRSVADTLROKVEDAVREHPDYRVVFTGHSLSGLGALATVAGADLRNGYD 187
QY 174 IRLYTFGEPRSGNOAFASYMNDAPQASSPDITQ-----YFRVTHANDGIPNLPPEQGYAH 229
DB 188 IDVFSYGAPRVGNRAFAEFL-----TVQTGGTLRYITHNTDIVRPLPPREFGYSH 237
QY 230 GGVEYW-----SVDPSYAQNTFVCTGDEVQCEAQQGGVNN-----AHTTYFGMTSGAC 279
DB 238 SSPEYIKSGTLVPVT-RNDIV-----KIEGIDATGNNQNPIDIPAHLWTFGLI-GTC 290
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238 SSEYWIKSTGLVPVT-RNDIV-----KIEGIDATGNNQNPDPDIPAHLWYFGLI-GTC 290

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RESULT 12
US-08-479-275D-2
; Sequence 2, Application US/08479275D
; Patent No. 5869438
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Patkar, Shankant A.
; APPLICANT: Gormsen, Erik
; APPLICANT: Clausen, Ib G.
; APPLICANT: Okkels, Jens S.
; APPLICANT: Thellersen, Marianne
; TITLE OF INVENTION: LIPASE VARIANTS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 58694380 No. 5869438disk of No. 5869438th America, Inc
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,275D
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3520.514-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO. 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-479-275D-2
;
; Query Match 23.7%; Score 353.5; DB 2; Length 291;
; Best Local Similarity 31.4%; Pred. No. 1.6e-28;
; Matches 94; Conservative 54; Mismatches 100; Indels 51; Gaps 1

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Qy	14	VTRAGHALAAS--TQGISEDLYSRLVEMATISQAAAYADL-----CNIPST-----IIKG	59
Dd	10	VSAMTALASPIRREVSQDLFNQFNLFAQYSAAYCGKNDAPAGTNITCTGNACPEVEKA	69
Qy	60	EKIY-----NSQTIDINGMILRDDSSKEIITVFRTGSDTNLQLDNTYTLPFDTLPCQN	117
Dd	70	DATFLYSPEDSGVDVTGFALDNTNKLIIVLSFRGRSRIENWIGNLPDLKEINDI---CS	127
Qy	114	GCEVHGYYIGHVSVQDVQVESLVKKOVSQYPDYALTVTGHSLGASLAALTAQAOLSATYDN	177
Dd	128	GCKRGHDGFTSWRSRVADTLQRKVQEDAVRKHDPDYRVVFTGHSUGGALATVAGADLRNGYD	187
Qy	174	IRLYTEGPBRSGNQAFASYMNDFAOSSPDDTQQ-----YFRVTHANDGIPLNPVEQGYAH	227
Dd	188	IDVESYGAPRVGNRAFAEPL-----TVQTGGTLYRITHTTNDIVPRLPFPREFGVSH	237
Qy	230	GGVEYW-----SVPDPSAQNTFYCTGDVEQCEAOGGQGVNN-----AHTTYFGMTSGAC	279
Dd	238	SSEPYWKSGTLVPVT-RNDIV----KIEGIDATGNNQPNIPIPAHLVTFGLI-GTC	290

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RESULT 13
US-08-488-271B-2
; Sequence 2, Application US/08488271B
; Patent No. 5892013
; GENERAL INFORMATION:
; APPLICANT: SVENDSEN, Allan
; APPLICANT: PATKAR, Shankant A.
; APPLICANT: GORMSEN, Erik
; APPLICANT: CLAUSEN, Ib G.
; APPLICANT: OKKELS, Jens S.
; APPLICANT: THELLERSEN, Marianne
; TITLE OF INVENTION: LIPASE VARIANTS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 58920130 No. 5892013disk of No. 5892013th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,271B
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3520.504-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-271B-2

Query Match      23.7%; Score 353.5; DB 2; Length 291;
Best Local Similarity 31.4%; Pred. No. 1.6e-28;
Matches 94; Conservative 54; Mismatches 100; Indels 51; Gaps 12;

Qy 14 VTAGHALAAS-TQIGSEDLVSRVEMATISOAAAYADL-----CNIPST-----IIKG 59
Db 10 VSAWTLASPIREVSQDLFNQNFQYSAAYCGKNDAPAGTNITCTGNACPEVEKA 69

Qy 60 EKIV-----NSQTDINGWILRDDSSKEIITVFRGTGSDTNLQDNTNLTPTPDLPCQN 113
Db 70 DATFLYSFEDSGVDVTGFLALDNTNKLIVLSFRGSRSIENWIGNLFDLKEINDI--CS 127

Qy 114 GCEVHGYYIGWVSQDVQVSVKQVQVDPYALTVTGHSLGASLAALTAQOLSATYDN 173
Db 128 GCRGHDGFTSWRSVADTLRQKVEDAVREHPDYRVVFTGHSLGALATVAGADLRNGYD 187

Qy 174 IRLYTFGEPRSGNOAFASYNDAPQASSPDQTQ-----YFRVTHANDGIPNLPVPGQYAH 229
Db 188 IDVFSYGAPRVGNRAFAEFL-----TVQGTGLYRITHNTNDIVPRLPREFGYSH 237

Qy 230 GGVEYV----SVDPSYAQNTFVCTGDEVQCEAGGQGVNN-----AHTTYFGMTSGAC 279
Db 238 SSPEYIKSGTLVPVT-RNDIV-----KIEGIDATGGNNQNPIDIPAHLYWFGLI-GTC 290

RESULT 14
US-08-140-008A-2
; Sequence 2, Application US/08140008A
; Patent No. 5914306
; GENERAL INFORMATION:
; APPLICANT: SVENDSEN, Allan
; APPLICANT: CLAUSEN, Ib
; APPLICANT: OKKELS, Jens
; APPLICANT: THELLERSEN, Marianne
; TITLE OF INVENTION: STABILIZED ENZYMES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 59143060 No. 5914306disk of No. 5914306th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/140,008A
; FILING DATE: 22-OCT-1993
; CLASSIFICATION: 252
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3601.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 867-0123
; TELEFAX: (212) 878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-140-008A-2

Query Match      23.7%; Score 353.5; DB 2; Length 291;
Best Local Similarity 31.4%; Pred. No. 1.6e-28;
Matches 94; Conservative 54; Mismatches 100; Indels 51; Gaps 12;

Qy 14 VTAGHALAAS-TQIGSEDLVSRVEMATISOAAAYADL-----CNIPST-----IIKG 59
Db 10 VSAWTLASPIREVSQDLFNQNFQYSAAYCGKNDAPAGTNITCTGNACPEVEKA 69

Qy 60 EKIV-----NSQTDINGWILRDDSSKEIITVFRGTGSDTNLQDNTNLTPTPDLPCQN 113
Db 70 DATFLYSFEDSGVDVTGFLALDNTNKLIVLSFRGSRSIENWIGNLFDLKEINDI--CS 127

Qy 114 GCEVHGYYIGWVSQDVQVSVKQVQVDPYALTVTGHSLGASLAALTAQOLSATYDN 173
Db 128 GCRGHDGFTSWRSVADTLRQKVEDAVREHPDYRVVFTGHSLGALATVAGADLRNGYD 187

Qy 174 IRLYTFGEPRSGNOAFASYNDAPQASSPDQTQ-----YFRVTHANDGIPNLPVPGQYAH 229
Db 188 IDVFSYGAPRVGNRAFAEFL-----TVQGTGLYRITHNTNDIVPRLPREFGYSH 237

Qy 230 GGVEYV----SVDPSYAQNTFVCTGDEVQCEAGGQGVNN-----AHTTYFGMTSGAC 279
Db 238 SSPEYIKSGTLVPVT-RNDIV-----KIEGIDATGGNNQNPIDIPAHLYWFGLI-GTC 290

RESULT 15
US-08-701-339-2
; Sequence 2, Application US/08701339
; Patent No. 5976855
; GENERAL INFORMATION:
; APPLICANT: SVENDSEN, Allan
; APPLICANT: CLAUSEN, Ib
; APPLICANT: OKKELS, Jens
; APPLICANT: THELLERSEN, Marianne

```

;; TITLE OF INVENTION: A Method of Preparing A Variant of A
;; TITLE OF INVENTION: Lipolytic Enzyme
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: No. 59768550 No. 5976855disk of No. 5976855th America, Inc.
;; STREET: 405 Lexington Avenue, 64th Floor
;; CITY: New York
;; STATE: New York
;; COUNTRY: United States of America
;; ZIP: 10174-6401
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/701,339
;; FILING DATE: 22-AUG-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lambiris, Elias J.
;; REGISTRATION NUMBER: 33,728
;; REFERENCE/DOCKET NUMBER: 4153.204-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-867-0123
;; TELEFAX: 212-878-9655
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 291 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-701-339-2

Query Match 23.7%; Score 353.5; DB 2; Length 291;
Best Local Similarity 31.4%; Pred. No. 1.6e-28;
Matches 94; Conservative 54; Mismatches 100; Indels 51; Gaps 12;

QY 14 VTAGHALAAS-TQGISIEDLYSLVEMATISQAAYADL-----CNIPST-----IIKG 59
DB 10 VSAWTALASPIREVSQDLFNQFNLFQAQYSAAYCGKNDAPAGTNTCTGNACPEVEKA 69
QY 60 EKII-----NSQTDINGWILRDDSSKEIITVPRGTGSDTNLQLDNTNYLTPTDTLPQC 113
DB 70 DATFLYSFEDSGVDVTGFLALDNTNKLIVLSFRGSRSIENWICNLNFDLKEINDI--CS 127
QY 114 GCEVHCYYIGVSVQDOVESLVKQVQYQVDPYALVTGHSIGASLAALTAQOLSATYDN 173
DB 128 GCRGHDGFTSSWRKSVADTLQRKVEDAVREHPDYRVVFTGHSIGALATVAGADLRNGYD 187
QY 174 IRLYTFGEPRSGNQAFASYNDAFOASSPDTTQ----YFRVTHANDGIPNLPPVQGYAH 229
DB 188 IDVFSYGARVGNRAAEFL-----TVTGGTLYRITHNDIVPLPRPFGYSH 237
QY 230 GGVEYH-----SVDPYSAQNTFVCTGDEVQCCGQGVNN-----AHTTYFGMTSGAC 279
DB 238 SSPEYWKSGTLVPVT-RNDIV---KIEGIDATGNNQNPNIPIPAHLWYFGLI-GTC 290

Search completed: December 17, 2003, 15:43:37
Job time : 22 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2003, 15:28:24 ; Search time 41 Seconds
(without alignments)
1087.858 Million cell updates/sec

Title: US-09-991-209-2

Perfect score: 1492

Sequence: 1 MKQFSAKHLVAVVTAGHAL.....QGVNNAHTYFGMTSGACTW 281

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1492	100.0	281 19	Aspergillus niger
2	1026	68.8	197 19	Aspergillus niger
3	403	27.0	77 17	Ferulic acid ester
4	368.5	24.7	295 19	Aspergillus oryzae
5	362	24.3	289 18	Product of Humicola
6	362	24.3	289 18	Humicola lanuginos
7	361	24.2	269 23	Thermomyces lanugi
8	360	24.1	269 23	Thermomyces lanugi
9	359.5	24.1	291 13	Humicola lanuginos

10	357	23.9	269	23	ABG32566	Thermomyces lanugi
11	356	23.9	269	23	ABG32565	Thermomyces lanugi
12	356	23.9	269	23	ABG32584	Thermomyces lanugi
13	356	23.9	269	23	ABG32602	Thermomyces lanugi
14	355.5	23.8	291	13	AAAR22640	Humicola lanuginos
15	355.5	23.8	291	13	AAAR22641	Humicola lanuginos
16	355.5	23.8	291	15	AAAR65400	Variant lipase E56
17	354.5	23.8	291	13	AAAR22631	Humicola lanuginos
18	354.5	23.8	291	13	AAAR22645	Humicola lanuginos
19	354.5	23.8	291	15	AAAR65416	Variant lipase D96
20	354.5	23.8	291	15	AAAR65417	Variant lipase L25
21	354	23.7	269	23	ABG32554	Thermomyces lanugi
22	354	23.7	269	23	ABG32560	Thermomyces lanugi
23	354	23.7	269	23	ABG32561	Thermomyces lanugi
24	354	23.7	269	23	ABG32563	Thermomyces lanugi
25	353.5	23.7	291	13	AAAR22633	Generic sequence o
26	353.5	23.7	291	13	AAAR22642	Humicola lanuginos
27	353.5	23.7	291	14	AAAR37878	Sequence of pre-pr
28	353.5	23.7	291	15	AAAR65444	Variant lipase D37
29	353.5	23.7	291	15	AAAR65447	Variant lipase D96
30	353.5	23.7	291	15	AAAR65449	Variant lipase E56
31	353.5	23.7	291	15	AAAR65412	Variant lipase D96
32	353.5	23.7	291	15	AAAR65413	Variant lipase D96
33	353.5	23.7	291	15	AAAR65415	Variant lipase D96
34	353.5	23.7	291	15	AAAR65418	Variant lipase L25
35	353.5	23.7	291	15	AAAR65419	Variant lipase L25
36	353.5	23.7	291	15	AAAR65420	Variant lipase L25
37	353.5	23.7	291	15	AAAR65421	Variant lipase L25
38	353.5	23.7	291	15	AAAR65423	Variant lipase L25
39	353.5	23.7	291	15	AAAR65424	Variant lipase L25
40	353.5	23.7	291	15	AAAR65426	Variant lipase L25
41	353.5	23.7	291	15	AAAR65396	Variant lipase E56
42	353.5	23.7	291	15	AAAR65397	Variant lipase E56
43	353.5	23.7	291	15	AAAR65398	Variant lipase E56
44	353.5	23.7	291	15	AAAR65399	Variant lipase E56
45	353.5	23.7	291	15	AAAR65401	Variant lipase E56

ALIGNMENTS

RESULT 1

AAW56728

ID AAW56728 standard; Protein; 281 AA.

AC AAW56728;
DT 28-AUG-1998 (first entry)

DE Aspergillus niger ferulic acid esterase.
KW Ferulic acid esterase; esterolytic enzyme; feed supplement;
KW fabric; yarn; textile.

OS Aspergillus niger.
XX WO9814594-A2.

XX 09-APR-1998.

XX 29-SEP-1997; 97WO-US17614.

XX 30-SEP-1996; 96US-0722713.

XX (GENV) GENENCOR INT INC.

XX Borneman WS, Bower BS;

XX WPI; 1998-240093/21.

XX N-PSDB; AAW28496.

XX New esterase from Aspergillus niger - useful for, e.g. feed and food processing, treating fabrics or for producing antioxidant.

PT photoprotective or antiinflammatory agents
 PS Claim 8; Fig 5A-B; 40pp; English.
 XX
 CC This polypeptide comprises a novel 38 kDa methyl ferulate esterase
 CC (FAE) of *Aspergillus niger*. Its amino acid sequence was deduced
 CC from a 2436 bp genomic DNA sequence (see AAV28496). The invention
 CC provides vectors that include the DNA sequence, host cells
 CC transformed with the DNA or vectors, fermentation broths comprising
 CC such host cells, and esterase proteins expressed by the host cells.
 CC The FAE can cleave the ester linkage of phenolic esters. It can be
 CC used in a claimed feed supplement and in a claimed process of
 CC treating fabric, yarn or textiles. It can also be used in the pulp
 CC and paper industry, for the synthesis of carbohydrate derivatives
 CC and in the bioconversion of agricultural residue to fermentable
 CC sugars and free phenolic acid useful e.g. as an antioxidant,
 CC photoprotective, antimicrobial or antiinflammatory agent in foods
 CC and personal care products, feedstock for conversion to flavours
 CC (e.g. vanillin), biopolymers and valuable chemicals. It can also
 CC be used in the modification of polysaccharides, e.g. gums, to
 CC generate new properties, and in the processing of grain.
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 1492; DB 19; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.6e-130; Mismatches 0; Indels 0; Gaps 0;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKQFSKXHLVAVVVTAGHALAASTQGISDLYSRLVEMATISQAAYADLCNIPSTIIKGE 60
 DB 1 MKQFSKXHLVAVVVTAGHALAASTQGISDLYSRLVEMATISQAAYADLCNIPSTIIKGE 60
 QY 61 KIYNSQTDINGWILRDDSSKEIITVPRGSGDNLQLDNTYLTTPDPTLPQCNGCEVHGG 120
 DB 61 KIYNSQTDINGWILRDDSSKEIITVPRGSGDNLQLDNTYLTTPDPTLPQCNGCEVHGG 120
 QY 121 YVIGWVSQDOVESLVKQVSDYALVTGHSGLASLAALTAQLSATYDNIIRLYTFG 180
 DB 121 YVIGWVSQDOVESLVKQVSDYALVTGHSGLASLAALTAQLSATYDNIIRLYTFG 180
 QY 181 EPRSGNQAFASYMNDFAQSSPDTTQYFRVTHANDGIPNLPVVEQYAHGGVEYWSVDPY 240
 DB 181 EPRSGNQAFASYMNDFAQSSPDTTQYFRVTHANDGIPNLPVVEQYAHGGVEYWSVDPY 240
 QY 241 SAQNTFVCTGDEVQCEAQQGGVNNAHITYFGMTSGACTW 281
 DB 241 SAQNTFVCTGDEVQCEAQQGGVNNAHITYFGMTSGACTW 281
 RESULT 2
 AAW56727
 ID AAW56727 standard; Protein; 197 AA.
 AC AAW56727;
 XX
 DT 28-AUG-1998 (first entry)
 DE *Aspergillus niger* ferulic acid esterase fragment.
 KW Ferulic acid esterase; esterolytic enzyme; feed supplement;
 KW fabric; yarn; textile.
 XX
 OS *Aspergillus niger*.
 XX
 PN WO9814594-A2.
 XX
 PD 09-APR-1998.
 XX
 PF 29-SEP-1997; 97WO-US17614.
 XX
 PR 30-SEP-1996; 96US-0722713.
 XX
 PA (GENEV) GENENCOR INT INC.

XX Borneman WS, Bower BS;
 XX
 DR WPI; 1998-240093/21.
 DR N-PSDB; AAV28495.
 XX
 PT New esterase from *Aspergillus niger* - useful for, e.g. feed and food
 PT processing, treating fabrics or for producing antioxidant,
 PT photoprotective or antiinflammatory agents
 XX
 XX Example 2; Fig 2; 40pp; English.
 PS
 CC This polypeptide comprises a portion of a novel 38 kDa methyl
 CC ferulate esterase (FAE, see AAW56728) of *Aspergillus niger*. Its
 CC amino acid sequence was deduced from a 650 bp DNA fragment (see
 CC AAV28495) obtained by PCR amplification of *A. niger* genomic DNA.
 CC The FAE can cleave the ester linkage of phenolic esters. It
 CC can be expressed in host cells and used in a claimed feed
 CC supplement and in a claimed process for treating fabric, yarn or
 CC textiles.
 XX
 SQ Sequence 197 AA;
 Query Match 68.8%; Score 1026; DB 19; Length 197;
 Best Local Similarity 100.0%; Pred. No. 3.5e-87;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 22 ASTQGISDLYSRLVEMATISQAAYADLCNIPSTIIKGEKIYNSQTDINGWILRDDSSKE 81
 DB 1 ASTQGISDLYSRLVEMATISQAAYADLCNIPSTIIKGEKIYNSQTDINGWILRDDSSKE 60
 QY 82 IITVFRGSGDNLQLDNTYLTTPDPTLPQCNGCEVHGGYIIGWVSQDOVESLVKQOVS 141
 DB 61 IITVFRGSGDNLQLDNTYLTTPDPTLPQCNGCEVHGGYIIGWVSQDOVESLVKQOVS 120
 QY 142 QYPDYALVTGHSGLASLAALTAQLSATYDNIIRLYTFGPRSGNQAFASYMNDFAQSS 201
 DB 121 QYPDYALVTGHSGLASLAALTAQLSATYDNIIRLYTFGPRSGNQAFASYMNDFAQSS 180
 QY 202 PDDTQYFRVTHANDGIP 218
 DB 181 PDDTQYFRVTHANDGIP 197
 RESULT 3
 AAW19713
 ID AAW19713 standard; peptide; 77 AA.
 AC AAW19713;
 XX
 DT 04-AUG-1997 (first entry)
 DE Ferulic acid esterase fragment #4.
 XX
 KW Ferulic acid esterase; FAE; enzyme system; plant; wheat bran; sugar beet;
 KW water insoluble pentosan; corn cobs; dough; lignin; terpenoid; vanillin;
 KW antioxidant; oxidative agent stabiliser; enzyme; cell wall breakdown;
 KW nutrient absorption; growth rate; feed utilisation; xylanase.
 XX
 OS *Aspergillus niger* strain 3M43.
 XX
 PN GB2301103-A.
 XX
 PD 27-NOV-1996.
 XX
 PF 23-MAY-1995; 95GB-0010370.
 XX
 PR 23-MAY-1995; 95GB-0010370.
 XX
 PA (DANI-) DANISCO AS.
 XX
 PI De Vries RP, Michelsen B, Poulsen CH, Soe JB, Visser J;
 PI Zargahi MR;

XX (NOVO) NOVO-NORDISK AS.
XX Fuglsang CC, Halkier T, Jorgensen ST, Okkels JS;
XX PI Patkar SA, Petersen DA, Thellersen M, Vind J;
XX DR WPI; 1997-132621/12.
XX DR N-PSDB; AAT68728.
XX Modified lipolytic enzymes with peptide extensions at one or both
PT ends - esp. for use in detergent and dishwashing compsn., have
PT improved substrate affinity, stability and wash performance
XX Example 5; Fig 3; 197pp; English.
XX The present sequence is the product of the coding region of the
CC Humicola lanuginosa lipase gene as present in the E. coli
CC expression vector pSX581. The signal sequence is the Aspergillus
CC lyticus protease I signal and Glu21 is the 1st amino acid residue
CC of the parent lipase.
XX SQ Sequence 289 AA;
Query Match 24.3%; Score 362; DB 18; Length 289;
Best Local Similarity 30.2%; Pred. No. 3.6e-25;
Matches 92; Conservative 58; Mismatches 105; Indels 50; Gaps 11;
QY 7 KHLVAVVTVAGHALAASTQGISDLYSLVEMATISQAAYADL-----CNIPST---- 55
DB 2 KRICGSLLLGLSISAALAEVSQDLFNQFNLPAQYSAAAYCGKNNDAPAGTNTICTGNAC 61
QY 56 --IIGKEKIY-----NSQTDINGWILRDDSSKEITVFRGTGSDTNLQDNTYLTTPFD 107
DB 62 PEVEKADATFLYSFEDSGVGDVTGFLALDNTNKLIVLSFRGSRSIENWIGNLNFDLKEIN 121
QY 108 TLPQNGCEVHGYYIGWVSQDQVESLVKQVSOYQPDYALTVTGHSLSGLASLAALTAQAL 167
DB 122 DI--CSGCRGHGFTSSWSRVADTLKQKVEDAVREHPDYRVVFTGHSLSGLALATVAGADL 179
QY 168 SATYDNIRLYTFGEPRSGNOAFASYMNDAPQASSPDTTQ-----YFRVTHANDGIPNLPV 223
DB 180 RGNVDIDVPSYGAPRVGNRAFAEFL-----TVQTGGTLYRITHNDIVRPLPPR 229
QY 224 EOGYANGGVVEYW-----SVDPYSQNTFVCTGDEVQCEAOGGQGVNN-----AHTTYFGM 274
DB 230 EFGYSHSSPEYWKSGTLVPVT-RNDIV-----KIEGIDATGNNQNPIDIPAHLMYFGL 284
QY 275 TSGAC 279
DB 285 I-GTC 288

RESULT 6
ID AAW19647
XX AAW19647 standard; Protein; 289 AA.
XX AC AAW19647;
XX 04-SEP-1997 (first entry)
XX Humicola lanuginosa modified lipase.
XX Lipase; lipolytic enzyme; protein engineering; detergent;
XX psX581.
XX Chimeric Humicola lanuginosa DSM4109;
XX Chimeric Aspergillus lyticus;
XX Key Location/Qualifiers
XX 1..20
FT Peptide /label= Sig_peptide
FT /note= "A. lyticus protease I signal"
FT 21..289
FT Protein

PT PT /label= Mat_protein
XX XX /note= "native mature enzyme"
XX NO9704079-A1.
XX PD 06-FEB-1997.
XX XX 12-JUL-1996; 96WO-DK00322.
XX 07-MAY-1996; 96US-0020461.
PR 14-JUL-1995; 95DK-0000832.
PR 13-SEP-1995; 95DK-0001013.
PR 29-SEP-1995; 95DK-0001096.
PR 21-NOV-1995; 95DK-0001306.
PR 14-FEB-1996; 96US-0011634.
PR 01-APR-1996; 96DK-0000372.
XX (NOVO) NOVO-NORDISK AS.
XX Fuglsang CC, Halkier T, Jorgensen ST, Okkels JS;
XX PI Patkar SA, Petersen DA, Thellersen M, Vind J;
XX WPI; 1997-132622/12.
XX DR N-PSDB; AAT68728.
XX Modified lipolytic enzymes with peptide extensions at one or both
PT ends - useful in detergent and dishwashing compsn., have improved
PT substrate affinity, stability and wash performance
XX Example 4; Fig 3; 191pp; English.
XX A modified lipase (AAW19647) comprises an Aspergillus lyticus
CC protease I signal and the mature protein sequence of Humicola
CC lanuginosa lipase. It is encoded by a DNA sequence (AAT68728)
CC present in E. coli expression vector pSX581. E. coli W3110 lacI1
CC (pSX581) transformants produced a lipase that showed no improvement
CC in wash performance over the native H. lanuginosa enzyme. Addition
CC of an N-terminal 5-amino acid extension (see also AAW19646) improved
CC wash performance 2-fold.
XX SQ Sequence 289 AA;
Query Match 24.3%; Score 362; DB 18; Length 289;
Best Local Similarity 30.2%; Pred. No. 3.6e-25;
Matches 92; Conservative 58; Mismatches 105; Indels 50; Gaps 11;
QY 7 KHLVAVVTVAGHALAASTQGISDLYSLVEMATISQAAYADL-----CNIPST---- 55
DB 2 KRICGSLLLGLSISAALAEVSQDLFNQFNLPAQYSAAAYCGKNNDAPAGTNTICTGNAC 61
QY 56 --IIGKEKIY-----NSQTDINGWILRDDSSKEITVFRGTGSDTNLQDNTYLTTPFD 107
DB 62 PEVEKADATFLYSFEDSGVGDVTGFLALDNTNKLIVLSFRGSRSIENWIGNLNFDLKEIN 121
QY 108 TLPQNGCEVHGYYIGWVSQDQVESLVKQVSOYQPDYALTVTGHSLSGLASLAALTAQAL 167
DB 122 DI--CSGCRGHGFTSSWSRVADTLKQKVEDAVREHPDYRVVFTGHSLSGLALATVAGADL 179
QY 168 SATYDNIRLYTFGEPRSGNOAFASYMNDAPQASSPDTTQ-----YFRVTHANDGIPNLPV 223
DB 180 RGNVDIDVPSYGAPRVGNRAFAEFL-----TVQTGGTLYRITHNDIVRPLPPR 229
QY 224 EOGYANGGVVEYW-----SVDPYSQNTFVCTGDEVQCEAOGGQGVNN-----AHTTYFGM 274
DB 230 EFGYSHSSPEYWKSGTLVPVT-RNDIV-----KIEGIDATGNNQNPIDIPAHLMYFGL 284
QY 275 TSGAC 279
DB 285 I-GTC 288

RESULT 7
ABG22582

XX New variants of fungal lipolytic enzymes with improved thermostability
PT useful for hydrolysing a carboxylic ester, controlling pitch troubles
PT in mechanical pulp production or paper-making process and for preparing
PT dough
XX
XX
XX Claim 10; Page -: 29pp; English.
XX
XX The present invention relates to a new variant of a parent fungal
CC lipolytic enzyme. The invention comprises an amino acid sequence
CC compared to the parent lipolytic enzyme comprises substitution of an
CC amino acid residue and which is more thermostable than the parent
CC lipolytic enzyme. The invention is useful for hydrolysing a carboxylic
CC acid ester, by incubating the ester with the lipase in the presence of
CC water, and for controlling pitch troubles in a process for the production
CC of mechanical pulp or a paper-making process using mechanical pulp. The
CC invention is also useful for preparing a dough or a baked product
CC prepared from the dough, and for hydrolysing, synthesising or
CC interesterifying as ester, by reacting the ester with water, reacting an
CC acid with an alcohol or interesterifying the ester with an acid, an
CC alcohol or a second ester in the presence of the invention, and also for
CC enzymatic removal of hydrophobic esters from fabrics. The invention is
CC further useful for preparing a baked product, e.g. pasta or noodles, as a
CC detergent additive and in leather industry. The invention is at least 4
CC plusOC more thermostable than the parent lipolytic enzyme. The addition
CC of the invention improves crumb structure of the baked product, and dough
CC properties e.g. a less soft dough, higher elasticity and lower
CC extensibility. The present amino acid sequence represents a Thermomyces
CC lanuginosus lipolytic enzyme variant of the invention.
CC Note: The present sequence is not shown in the specification but is
CC derived from the Thermomyces lanuginosus lipolytic enzyme (ABG32551)
CC sequence given on pages 20-21 of the specification.
XX
SQ Sequence 269 AA;
Query Match 24.1%; Score 360; DB 23; Length 269;
Best Local Similarity 31.7%; Pred. No. 4.9e-25;
Matches 90; Conservative 48; Mismatches 98; Indels 48; Gaps 10;
QY 27 ISEDLYSRVEMATISQAAYADL-----CNIPST-----IIRGEKIY-----NSQT 67
DB 2 VSQDLFNQFNLAQYSAAYCGKNNAPAGTNTCTGNACPEVEKADATFLYSPEDSGVG 61
QY 68 DINGWILRDDSKKEIITVRGTGSDTNLQDNTNYTLTPPDTLPQCNGCEVHGYYIGWVS 127
DB 62 DVTGFLALDNTNKLIVLSFRGSRSIENWICNLFNLDLKEINDI--CSGCRGHGGFTSSWRS 119
QY 128 VQDQVESLVKQVQSYQPDYALVTGHSGLASLAALTAQALSATYDNLRLTYFGEPSGNQ 187
DB 120 VADTLRQKVEDAVREHPDYRVVFTGHSGLGALATVAGADLRGNGYDIDVPSGAPRVGNR 179
QY 188 AFASYMNDFAQASSPDTTQ----YFRVTHANDGIPNLPPVEQYAHGGVYEVSWDPYS-- 241
DB 180 AFAEFL-----TVGTGGTLYRTHINDIVRLPPREFGYSHPSPYEWIKSPGTGVP 229
QY 242 -AQTFTVCTGDEVQCEAGCGGVNN-----AHTTYFGMTSGAC 279
DB 230 VTRNDIV-----KIEGIDATGNNQNPIDPITAHLWTFGLI-GTC 268
RESULT 9
AAR22643
ID AAR22643 standard; Protein; 291 AA.
XX
AC AAR22643;
XX
DT 25-MAR-2003 (updated)
DT 06-OCT-1992 (first entry)
XX
DE Humicola lanuginosa lipase type III variant.
XX
KW Catalytic triad; trypsin; binding pocket; mutation; detergent; HLL.
XX

OS Humicola lanuginosa.
XX Key Location/Qualifiers
FH 1..22 /note= "signal peptide of pre-pro-lipase"
FT Misc-difference 281
FT /label= Leu-> Thr.
FT /note= "indicated as position 259 in the patent"
XX
XX W09205249-A.
FN 02-APR-1992.
XX 12-SEP-1991; 91WO-US06605.
XX 13-SEP-1990; 90DK-0002194.
PR 13-SEP-1990; 90DK-0002195.
PR 13-SEP-1990; 90DK-0002196.
XX (NOVO) NOVO-NORDISK AS.
PA Svendsen A, Clausen I, Packar SA, Gormsen E;
XX WPI; 1992-132120/16.
XX Variant lipases with critical residues substd. or deleted -
XX confers different hydrophobicity or electrostatic properties on
XX binding pocket of enzyme contg. catalytic triad
XX Claim 50; Page 51; 71pp; English.
XX The sequence shows a lipase type III variant comprising a trypsin-like
XX catalytic triad including an active site serine located in a
XX predominantly hydrophobic, elongated binding pocket; and a surface
XX loop structure which covers the active site serine when the lipase is
XX in its inactive conformation and changes occur when the lipase is
XX activated to make the serine accessible to the lipid substrate, the
XX loop having a predominantly hydrophobic inner surface facing the
XX binding pocket and a primarily hydrophilic outer surface. The
XX variant is characterised by a substitution of Thr for Leu
XX in the loop structure (see feature table). The position of the
XX mature sequence of the lipase from Humicola lanuginosa strain
XX DSM 4106. However, the sequence given in the specification and
XX reproduced here is that of the pre-pro amino acid sequence of HLL
XX produced from the expression plasmid p960. Mutations were indicated
XX using this sequence as a base but discrepancies may occur between
XX residues stated in the patent and those indicated in the sequence.
XX The lipase variants have altered specificities and/or improved
XX properties, particularly w.r.t. accessibility of the active site
XX serine, and may be used as detergent additives.
XX See also AAR22629-45.
XX (Updated on 25-MAR-2003 to correct PA field.)
XX (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 291 AA;
Query Match 24.1%; Score 359.5; DB 13; Length 291;
Best Local Similarity 31.8%; Pred. No. 6.1e-25;
Matches 95; Conservative 54; Mismatches 99; Indels 51; Gaps 12;
QY 14 VTAGHALAAS-TGISEDLYSRVEMATISQAAYADL-----CNIPST-----IIRG 59
DB 10 VSAWTAALASPIRREVSDQLFNQFNLAQYSAAYCGKNNAPAGTNTCTGNACPEVEKA 69
QY 60 EKIY-----NSQTDINGWILRDDSKKEIITVRGTGSDTNLQDNTNYTLTPPDTLPQC 113
DB 70 DATFLYSPEDSGVGDVTGFLALDNTNKLIVLSFRGSRSIENWICNLFNLDLKEINDI--CS 127
QY 114 GCEVHGYYIGWVSQDQVESLVKQVQSYQPDYALVTGHSGLASLAALTAQALSATYDN 173
DB 128 GCRGHGGFTSSWRSVADTLRQKVEDAVREHPDYRVVFTGHSGLGALATVAGADLRGNGYD 187

Qy 174 IRLYTFGPRGNOAPASYMNDFAQASPDITQ-----YFRVTHANDGIPNLPPVQGYAH 229
 Db 188 IDVESYGAPVGNRAFAEFL-----TVQTGGLYRIHTNDIVRLPFRFGYSH 237
 Qy 230 GGVEW-----SVDPYSAQNTFVCTGDEVQCCRAQGGQVNN-----AHTTYFGMTSGAC 279
 Db 238 SSPEYWIKSGTLVPVT-RNDIV-----KIEGIDATGNNQNPIDIPAHWTYFGLI-GTC 290

RESULT 10

ABG32566
 ID ABG32566 standard; Protein; 269 AA.

XX AC ABG32566;

XX AC (first entry)

DT 15-NOV-2002 (first entry)

XX Thermomyces lanuginosus lipolytic enzyme variant #14.

XX Fungal; lipolytic; enzyme; pitch trouble; mechanical pulp; paper-making;
 KW dough; baked product; fabric; pasta; noodle; detergent additive; leather;
 KW crumb structure; soft dough; elasticity; extensibility; variant.

XX Thermomyces lanuginosus.

XX Key Location/Qualifiers

FT Misc-difference 27 /note= "Asp substituted by Arg"

FT Misc-difference 111

FT Misc-difference 216 /note= "Asp substituted by Gly"

FT Misc-difference 216 /note= "Ser substituted by Pro"

FT Misc-difference 227 /note= "Leu substituted by Val"

FT Misc-difference 256 /note= "Pro substituted by Thr"

FT Misc-difference 256 /note= "Pro substituted by Thr"

FT Misc-difference 256 /note= "Pro substituted by Thr"

FT Misc-difference 256 /note= "Pro substituted by Thr"

FT Misc-difference 256 /note= "Pro substituted by Thr"

FT Misc-difference 256 /note= "Pro substituted by Thr"

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FT Misc-difference 256 /note= "Pro substituted by Thr"

FT Misc-difference 256 /note= "Pro substituted by Thr"

FT Misc-difference 256 /note= "Pro substituted by Thr"

FT Misc-difference 256 /note= "Pro substituted by Thr"

CC further useful for preparing a baked product, e.g. pasta or noodles, as a
 CC detergent additive and in leather industry. The invention is at least 4
 CC plusoc more thermostable than the parent lipolytic enzyme. The addition
 CC of the invention improves crumb structure of the baked product, and dough
 CC properties e.g. a less soft dough, higher elasticity and lower
 CC extensibility. The present amino acid sequence represents a Thermomyces
 CC lanuginosus lipolytic enzyme variant of the invention.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the Thermomyces lanuginosus lipolytic enzyme (ABG32551)
 CC sequence given on pages 20-21 of the specification.

XX SQ Sequence 269 AA;

Query Match 23.9%; Score 357; DB 23; Length 269;

Best Local Similarity 31.9%; Pred. No. 9.3e-25;

Matches 91; Conservative 50; Mismatches 94; Indels 50; Gaps 11;

Qy 27 ISEDIYSRLVENMATTISQAYADL-----CNIPST-----IIKGEKIY-----NSQT 67

Db 2 VSQDLFNQNLFAQYSAAYCGKNRAPAGTITCTGNACPEVEKADATFLYSPEDSGVG 61

Qy 68 DINGHILRDDSSKEIITVFRGTGSDTNLQDNTYLTTPDITLPCQNGCEVHGYYIGWVS 127

Db 62 DVTGFLALDNTNKLIVLSPGRSRIENWTGNLNFDLKEINDI--CSGCRGHGGFTSSWRS 119

Qy 128 VQDQVESLVKQOVSOYDYALVTGHSLSGASLAALTAOLSATYDNIIRLYTFEPESGNCQ 187

Db 120 VADTLRQKVEDAVREHPDYRVVFTGHSLSGALATVAGADLRGNGYDIDVFSYCAPRVGNR 179

Qy 188 AFASYMNDFAQASPDITQ-----YFRVTHANDGIPNLPPVQGYAHGGVEYH-----SVDP 239

Db 180 AFAEFL-----TWQTGGLYRIHTNDIVRLPFRFGYSHPSPEYWIKSGTVTP 229

Qy 240 YSAQNTFVCTGDEVQCCRAQGGQVNN-----AHTTYFGMTSGAC 279

Db 230 VT-RNDIV-----KIEGIDATGNNQNPIDIPAHWTYFGLI-GTC 268

RESULT 11

ABG32565
 ID ABG32565 standard; Protein; 269 AA.

XX AC ABG32565;

XX AC (first entry)

DT 15-NOV-2002 (first entry)

XX Thermomyces lanuginosus lipolytic enzyme variant #13.
 KW Fungal; lipolytic; enzyme; pitch trouble; mechanical pulp; paper-making;
 KW dough; baked product; fabric; pasta; noodle; detergent additive; leather;
 KW crumb structure; soft dough; elasticity; extensibility; variant.

XX Thermomyces lanuginosus.

XX Key Location/Qualifiers

FT Misc-difference 27 /note= "Asp substituted by Arg"

FT Misc-difference 111 /note= "Asp substituted by Gly"

FT Misc-difference 216 /note= "Asp substituted by Pro"

FT Misc-difference 227 /note= "Leu substituted by Phe"

FT Misc-difference 256 /note= "Pro substituted by Thr"

FT Misc-difference 256 /note= "Pro substituted by Thr"

FT Misc-difference 256 /note= "Pro substituted by Thr"

FT Misc-difference 256 /note= "Pro substituted by Thr"

FT Misc-difference 256 /note= "Pro substituted by Thr"

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FT Misc-difference 256 /note= "Pro substituted by Thr"

FT Misc-difference 256 /note= "Pro substituted by Thr"

FT Misc-difference 256 /note= "Pro substituted by Thr"

FT Misc-difference 256 /note= "Pro substituted by Thr"

FT Misc-difference 256 /note= "Pro substituted by Thr"

XX The present invention relates to a new variant of a parent fungal
 CC lipolytic enzyme. The invention comprises an amino acid sequence which
 CC compared to the parent lipolytic enzyme comprises substitution of an
 CC amino acid residue and which is more thermostable than the parent
 CC lipolytic enzyme. The invention is useful for hydrolysing a carboxylic
 CC acid ester, by incubating the ester with the lipase in the presence of
 CC water, and for controlling pitch troubles in a process for the production
 CC of mechanical pulp or a paper-making process using mechanical pulp. The
 CC invention is also useful for preparing a dough or a baked product
 CC prepared from the dough, and for hydrolysing, synthesising or
 CC esterifying as ester, by reacting the ester with water, reacting an
 CC acid with an alcohol or esterifying the ester with an acid, an
 CC alcohol or a second ester in the presence of the invention, and also for
 CC enzymatic removal of hydrophobic esters from fabrics. The invention is

Query Match		23.9%; Score 356; DB 23; Length 269;
Best Local Similarity		31.8%; Pred. No. 1.2e-24;
Matches		90; Conservative 47; Mismatches 100; Indels 46; Gaps 10;
QY	27	ISEDYSLVEMWATISQAYADL-----CNIPST-----IIKGEKIY-----NSQT 67
Db	2	VSQDLFNFLPAQYSAAYAAKGNRAPAGTITTCGNACPEVEKADATFLYSHFSDSGVG 61
QY	68	DINGWILRDDSSKEIITVPRGSGSDTNLQLDNTYLTLPDTPQNGCEVHGXYIGWVS 127
Db	62	DTGFLALDNTNKLIVLFRGSRSTENWTANLNFJLKEINDI--CGCRGHGGFTSSWS 119
QY	128	VQDQVESLVKQVQSPYDVALVTGHSGLASLAALTAQLSATYDNIIRLYTFGEPRSGNQ 187
Db	120	VADTLRQKVEDAVREHPDYRVFTGHSGLGALATVAGADLRNGYDIDVFSYGAPRVGNR 179
QY	188	APASVMNDAFOASSPDTTQ-----YFRVTHANDGIPNLPPVQGYAHGVEYVMSVDPYSAQ 243
Db	180	APAEPL-----TVQTGGLYRITHNTNDIVPLPRFRGYSHPSPEYMI--KSGT 226
QY	244	NTFVCTGD--EVOCCEAGGQGVNN-----AHTYFGMTSGAC 279
Db	227	GVPTNRDIVKIGIDATGGNNQNPIDITAHLYFGLI-GTC 268
RESULT 13		
ID	ABG32602	standard; Protein; 269 AA.
XX	AC	ABG32602;
XX	XX	
DT	15-NOV-2002	(first entry)
XX	DE	Thermomyces lanuginosus lipolytic enzyme variant #50.
XX	KW	Fungal; lipolytic; enzyme; pitch trouble; mechanical pulp; paper-making;
KW	KW	dough; baked product; fabric; pasta; noodle; detergent additive; leather;
KW	KW	crumb structure; soft dough; elasticity; extensibility; variant.
XX	OS	Thermomyces lanuginosus.
XX	XX	
FH	Key	Location/Qualifiers
FT	Misc-difference 27	/label= Asn, Arg, Ser
FT	Misc-difference 29	/note= "Pro substituted by Ser"
FT	Misc-difference 32	/note= "Thr substituted by Ser"
FT	Misc-difference 51	/label= Ile, Leu
FT	Misc-difference 76	/note= "Ile substituted by Val"
FT	Misc-difference 84	/note= "Arg substituted by Cys"
FT	Misc-difference 90	/label= Leu, Val
FT	Misc-difference 91	/label= Ala, Asn, Ser, Thr, Trp
FT	Misc-difference 93	/note= "Leu substituted by Phe"
FT	Misc-difference 94	/label= Lys, Arg, Ser
FT	Misc-difference 95	/note= "Phe substituted by Ile"
FT	Misc-difference 96	/label= Gly, Asn
FT	Misc-difference 101	/note= "Asn substituted by Asp"
FT	Misc-difference 111	/label= Arg, Gly
FT	Misc-difference 118	/note= "Arg substituted by Met"
FT	Misc-difference 131	
FT	Misc-difference 135	/note= "Ala substituted by Val"
FT	Misc-difference 137	/note= "His substituted by Tyr"
FT	Misc-difference 162	/note= "Asp substituted by Asn"
FT	Misc-difference 187	/note= "Asn substituted by Arg"
FT	Misc-difference 211	/note= "Val substituted by Ile"
FT	Misc-difference 216	/note= "Phe substituted by Tyr"
FT	Misc-difference 224	/note= "Ser substituted by Pro"
FT	Misc-difference 225	/label= Ile, Tyr
FT	Misc-difference 226	/note= "Gly substituted by Pro"
FT	Misc-difference 227	/note= "Thr substituted by Asn"
FT	Misc-difference 228	/label= Cys, Ile
FT	Misc-difference 238	/note= "Ile substituted by Val"
FT	Misc-difference 256	/note= "Pro substituted by Thr"
XX	WO200255679-A2.	
XX	18-JUL-2002.	
XX	10-JAN-2002; 2002WO-DK000016.	
XX	10-JAN-2001; 2001DK-00000032.	
XX	18-JAN-2001; 2001US-262579P.	
XX	(NOVO) NOVOZYMES AS.	
XX	Minning S, Vind J, Glad SOS, Danielsen S, Borch K;	
XX	WPI; 2002-619105/66.	
XX	New variants of fungal lipolytic enzymes with improved thermostability	
XX	useful for hydrolysing a carboxylic ester, controlling pitch troubles	
XX	in mechanical pulp production or paper-making process and for preparing	
XX	dough	
XX	Claim 20; Page -: 29pp; English.	
XX	The present invention relates to a new variant of a parent fungal	
XX	lipolytic enzyme. The invention comprises an amino acid sequence which	
XX	compared to the parent lipolytic enzyme comprises substitution of an	
XX	amino acid residue and which is more thermostable than the parent	
XX	lipolytic enzyme. The invention is useful for hydrolysing a carboxylic	
XX	acid ester, by incubating the ester with the lipase in the presence of	
XX	water, and for controlling pitch troubles in a process for the production	
XX	of mechanical pulp or a paper-making process using mechanical pulp. The	
XX	invention is also useful for preparing a dough or a baked product	
XX	prepared from the dough, and for hydrolysing, synthesising or	
XX	interesterifying as ester, by reacting the ester with water, reacting an	
XX	acid with an alcohol or interesterifying the ester with an acid, an	
XX	alcohol or a second ester in the presence of the invention, and also for	
XX	enzymatic removal of hydrophobic esters from fabrics. The invention is	
XX	further useful for preparing a baked product, e.g. pasta or noodles, as a	
XX	detergent additive and in leather industry. The invention is at least 4	
XX	plusC more thermostable than the parent lipolytic enzyme. The addition	
XX	of the invention improves crumb structure of the baked product, and dough	
XX	properties e.g. a less soft dough, higher elasticity and lower	
XX	extensibility. The present amino acid sequence represents a Thermomyces	
XX	lanuginosus lipolytic enzyme variant of the invention.	
XX	Note: The present sequence is not shown in the specification but is	

CC derived from the Thermomyces lanuginosus lipolytic enzyme (ABG32551)
 CC sequence given on pages 20-21 of the specification.
 XX
 SQ Sequence 269 AA;
 Query Match 23.9%; Score 356; DB 23; Length 269;
 Best Local Similarity 31.3%; Pred. No. 1.2e-24;
 Matches 89; Conservative 48; Mismatches 99; Indels 48; Gaps 10;
 QY 27 ISEDLYSLVEMATISQAAYADLCNIPST-----IIRGE--KIYNSQ----- 67
 DB 2 VSODLFNQFNLAQYSAAYCGKNYASAGSNITCTGNACPEVEKADATLYSPEDSGVG 61
 QY 68 DINGWILRDDSKKEIITVFRGTGSDTNLQDWTYTLTPPDTLPQCNGCEVHGYYLGGWS 127
 DB 62 DVTGFLALDNTNKLVLSPFGSCSIENWXXFXILKEIDDI--CSGRGHXGFTSWMS 119
 QY 128 VODOVESLVKQVSYQVDPYALVTGHSLGASLAALTAQALSATVDNIRLVTPGEPSSGNQ 187
 DB 120 VADTIRQKVEDVVRFPNTRVFTGHSLGALATVAGADLRGRGVDIDVPSYCAPRVGNR 179
 QY 188 AFASYNDFAQASSPDTTQ-----YFRVTHANDGIPNLPPVEQYAHGGVEYWSVDPYS-- 241
 DB 180 AFAEFL-----TIQTGGTLXRIHTNDIVPRLPPREYGVSHPSPEYWIKNXPX 229
 QY 242 -AQNTFVCTGDEVOCCEAOGQGVNN-----AHTTFVGMTSGAC 279
 DB 230 VTRNDIV-----KVEGIDATGNNQNPIDITAHLWYFGLI-GTC 268
 RESULT 14
 AAR22640
 ID AAR22640 standard; Protein; 291 AA.
 XX
 AC AAR22640;
 XX
 DT 25-MAR-2003 (updated)
 DT 06-OCT-1992 (first entry)
 XX
 DE Humicola lanuginosa lipase type III variant.
 XX
 KW Catalytic triad; trypsin; binding pocket; mutation; detergent; HLL.
 XX
 OS Humicola lanuginosa.
 FH Key Location/Qualifiers
 FT Peptide 1..22
 FT Misc-difference 108 /note= "signal peptide of pre-pro-lipase"
 FT /label= Ile-> Thr.
 FT /note= "indicated as position 86 in the patent"
 XX
 PN W09205249-A.
 XX
 PD 02-APR-1992.
 XX
 PF 12-SEP-1991; 91WO-US06605.
 XX
 PR 13-SEP-1990; 90DK-0002194.
 PR 13-SEP-1990; 90DK-0002195.
 PR 13-SEP-1990; 90DK-0002196.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Svendsen A, Clausen I, Patkar SA, Gormsen B;
 XX
 DR WPI; 1992-132120/16.
 XX
 XX Variant lipases with critical residues substd. or deleted -
 PT confers different hydrophobicity or electrostatic properties on
 PT binding pocket of enzyme contg. catalytic triad
 XX
 PS Claim 50; Page 51; 7lpp; English.

XX The sequence shows a lipase type III variant comprising a trypsin-like
 CC catalytic triad including an active site serine located in a
 CC predominantly hydrophobic, elongated binding pocket; and a surface
 CC loop structure which covers the active site serine when the lipase is
 CC in its inactive conformation and changes occur when the lipase is
 CC activated to make the serine accessible to the lipid substrate, the
 CC loop having a predominantly hydrophobic inner surface facing the
 CC binding pocket and a primarily hydrophilic outer surface. The
 CC variant is characterised by a substitution of Thr for Ile
 CC in the loop structure (see feature table). The position of the
 CC mutation given in the specification are assumed to use the
 CC mature sequence of the lipase from Humicola lanuginosa strain
 CC DSM 4106. However, the sequence given in the specification and
 CC reproduced here is that of the pre-pro amino acid sequence of HLL
 CC produced from the expression plasmid p960. Mutations were indicated
 CC using this sequence as a base but discrepancies may occur between
 CC residues stated in the patent and those indicated in the sequence.
 CC The lipase variants have altered specificities and/or improved
 CC properties, particularly w.r.t. accessibility of the active site
 CC serine, and may be used as detergent additives.
 CC See also AAR22629-45.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 291 AA;
 Query Match 23.8%; Score 355.5; DB 13; Length 291;
 Best Local Similarity 31.4%; Pred. No. 1.4e-24;
 Matches 94; Conservative 54; Mismatches 100; Indels 51; Gaps 12;
 QY 14 VTAGHALAAS-TGISEDLYSLVEMATISQAAYADL-----CNIPST-----IIRG 59
 DB 10 VSAWALASPIRREVSQDLFNQFNLAQYSAAYCGKNNDAPAGTNTCTGNACPEVEKA 69
 QY 60 EKIV-----NSQTDINGWILRDDSKKEIITVFRGTGSDTNLQDWTYTLTPPDTLP 113
 DB 70 DATFLVSFEDSGVGDVGTGFLALDNTNKLIVLSFRGSRSTENWGNLFDLKEINDI--CS 127
 QY 114 GCEVHGYYIGWVSQDVQVESLVKQVSYQVDPYALVTGHSLGASLAALTAQALSATVDN 173
 DB 128 GCRGHGDTSWRSVADTLRQKVEDAVREHPDYRVVFTGHSLGALATVAGADLRNGYD 187
 QY 174 IRLYTGEPSSGNQAFASYNDFAQASSPDTTQ-----YFRVTHANDGIPNLPPVEQYAH 229
 DB 188 IDVFSYGAPRVGNRAFAEFL-----TVQTGGTLXRIHTNDIVPRLPPREFGYSH 237
 QY 230 GGVEYW-----SVDPYSAQNTFVCTGDEVOCCEAOGQGVNN-----AHTTFVGMTSGAC 279
 DB 238 SSPEYWKSGTLVPVT-RNDIV-----KIEGIDATGNNQNPIDIPAHLWYFGLI-GTC 290
 RESULT 15
 AAR22641
 ID AAR22641 standard; Protein; 291 AA.
 XX
 AC AAR22641;
 XX
 DT 25-MAR-2003 (updated)
 DT 06-OCT-1992 (first entry)
 XX
 DE Humicola lanuginosa lipase type III variant.
 XX
 KW Catalytic triad; trypsin; binding pocket; mutation; detergent; HLL.
 XX
 OS Humicola lanuginosa.
 FH Key Location/Qualifiers
 FT Peptide 1..22
 FT Misc-difference 112 /note= "signal peptide of pre-pro-lipase"
 FT /label= Ile-> Thr.
 FT /note= "indicated as position 90 in the patent"

[illegible]